

Approved
1/14/03

6943277



GNCAGCATTTCCTCTAAGGGATNCAATNNGGCTTGCCCCGAGGCCACACTCATTTCCTCCCATNCCC
TCAAATACTGTGGTGATTAAACATTTTCATAGGAGGANTTTATGGATNCCTTTAAAANCCTAATT
CTCCCTGCTTGCCAAATCATTCTTCTCAGCATCCTGCCCAGCAAAAAANCANCTTNTGATCAA
AATNATCCCCGGAGGCTTNACGGAGGCCAGACCTGCCACAGCAGNAGTCCNGGAGATTGCTGAC
CGGGTCAAAGCACAGCTCGANGAGGAAACCAATGAGAAATATGAAATATTCAAAGCCGTTGAGT
ATAAACTCAAGTTGTCGCTGGAGTCAATTACTTCATTAAGATGGATGTAGGGGGTGGTTGTTT
CACCCACATAAAAGTCTTCAAGGATCTTTCTGGAAAGAATAATTTGGAACCTTACTGGTTACCAG
ACTAACAAAACCGAGGATGATGAGCTGACCTACTTCTAAGCAGCAAATTCTAAAGTGACCTGAT
TCCTCTCATTGTAACTGATTTCGNCCATCAATAAAGAATATTCTCCA (SEQ ID NO:1)

FIGURE 1

09/104180



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TECH CENTER 1600/2900

underlined = deleted in targeting construct

[] = sequence flanking Neo insert in targeting construct

[GNCAGCATTTCTCTAAGGGATNCAATNMGGCTTGCCCGAGGCCCACTCATTTCCTCCCA
 TNCCTCAAATACTGTGGTGATTAAACATTTTCATAGGAGGANTTTATGGATNCCTTTAAA
 ANCCTAATTCTCCCTGCTTGCCAAATCATTCTTCTCAGCATCCTGCCAGCAAAAAANC
 ANCTTNTGATCAAAATNATCCCCGAGGCTTNACGGAGGCCAGACCTGCCACAGCAGN]A
GTCNNGGAGATTGCTGACCGGGTCAAAGCACAGCTCGANGAGGAAACCAATGAGAAATAT
GAAATATTCAAAGCCGTTGAGTATAAACTCAAGTTGTCGCTGGAGTCAATTACTTCATT
AAGATGGATGTAGGGGGTGGTGTGTTTCACCCACATAAAAAGTCTTCAAGGATCTTTCTGGA
AAGAATAATTTGGAACCTTACTGGTTACCAGACTAACAAAACCGAGGATGATGAGCTGAC
 CTACTTCTAAGCAGCAAAATTCTAAAGTGACCTGATTCTCTCATTGTAAACTGATTCGNC
 CATCAATAAAGAATATTCTCCA]

Sub #8

FIGURE 2A

Approved
PB
1/14/07

OCT 28 2002

JCOB
DEMARK OFFICE**Gene Sequence
Structure***

238 bp

Sequence Deleted

436 bp

Size of EST: 559 bp

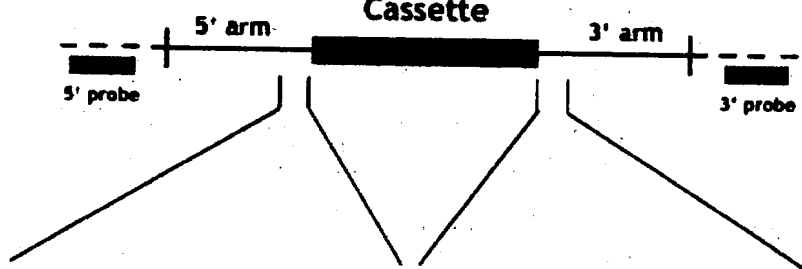
**Targeting Vector*
(genomic sequence)**

Construct Number: 2757

Arm Length:

5': 1.2 kb

3': 3 kb

**LacZ-Neo
Cassette**

———— Targeting Vector
 - - - - Endogenous Locus

* Not drawn to scale

5' > CGAGGCCACACTCATTTC
 ATTCCCTCAGATACTGTGATGATT
 ATACATTTGATAGGAGGAGATTAT
 GGATACCTTTAAAATTCTAAGTCT
 CCCTGCTTGCCAGATCATTCTTC
 TCAGCATTCTGCCCAGCAAAGAAG
 CAACTCGTGATCAGAATGATACCC
 GGAGGCTTGATGGAGGCCAGACCT
 GCCACAGCAGA < 3'
 (SEQ ID NO:2)

5' > ACTGGTTACCAGACTAACAAA
 ACCGAAGATGATGAAGTACCTAC
 TTCTAAGCAGCAAATTCATAAGTC
 ACCTGATTCCCTCTCATTGTAAACT
 GATGCGGCCATCAATAAAGAAATA
 TTCTTCAAATAAAAAAAAAAAGA
 AAGAAGCATTCTAACACAATACAA
 TCCAAAGATGTACTGATTTGATGT
 TACATACTCAG < 3'
 (SEQ ID NO:3)

FIGURE 2B